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<110> Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir

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<130> D-0021.5 PCT

<140> PCT/US99/24879

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<150> 09/177,776

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 Met Pro Val His Pro
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 <213> HUMAN

<400> 7
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<210> 8
 <211> 26
 <212> DNA
 <213> HUMAN

<400> 8
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<210> 9
 <211> 48

<212> DNA
<213> HUMAN

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<222> (1)..(48)
<223> anchor primer that anneals to the homopolymeric tail.

<220>
<221> inosine
<222> (36)..(37) (41)..(42) (46)..(47)
<223> each of the modified_bases at positions (36), (37), (41), (42), (46)
and (47) are inosine

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<400> 10
Glu Glu Asp Leu Pro Ser
1 5

<210> 11
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<400> 11
Gly Glu Asp Asp Pro Leu
1 5

<210> 12
<211> 21
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1 5 10 15

Tyr Gly Gly Asp Pro
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Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu
1 5 10 15

Pro Gly Glu Glu Asp Leu Pro Gly
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<210> 16
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<400> 16
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cacaccgtgt gctgggacac cccac 205

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<212> PRT
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<400> 22
Leu Glu His His His His His His
1 5

<210> 23
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<212> DNA
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<300>
<301> Locker and Buzard,
<303> DNA Sequencing and Mapping
<304> 1
<306> 3-11
<307> 1990

<400> 24
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<220>
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<223> sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989)
as motif frequently found in gene regulatory proteins.

<220>
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<222> (3)..(4)
<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as motif frequently found in gene regulatory proteins.

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<210> 26

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<213> HUMAN

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as a motif frequently found in gene regulatory proteins.

<220>
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<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as a motif frequently found in gene regulatory proteins.

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<220>
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<222> (1)..(540)

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acatgagctg ctttcctctc cagccagagg acatgggggg ccccagctcc cctgcctttc 180
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 gaggatctac ctggagagga ggatctacct gaagttaagc ctaaatacaga agaagagggc 360
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 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 2nd MN exon

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<210> 30
 <211> 171
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<220>
 <221> exon
 <222> (1)
 <223> 3rd MN exon

<400> 30
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<220>
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aaggccaccg tttccctgcc gag 143

<210> 32
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<213> HUMAN

<220>
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<223> 5th MN exon

<400> 32
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<210> 33
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<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 6th MN exon

<400> 33
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gaggaag 67

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<221> exon
<222> (1)
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<220>
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agcagtcctc gggctgctga gccag 145

<210> 36
<211> 27
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 9th MN exon

<400> 36
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<210> 37
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<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 10th MN exon

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tgcagatgag aaggcagcac ag 82

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<220>

<221> exon
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 <223> 11th MN exon

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<220>
 <221> intron

<222> (1)..(193)
<223> 2nd MN intron

<400> 40
gtgagacacc caccgctgc acagacccaa tctgggaacc cagctctgtg gatctccct 60
acagccgtcc ctgaacactg gtcccggcg tcccaccgc cggccaccgt cccacccct 120
caccttttct acccgggttc cctaagttcc tgacctaggc gtcagacttc ctcactatac 180
tctcccaccc cag 193

<210> 41
<211> 131
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

<400> 41
gtgaggggggt ctccccgccg agacttgggg atggggcggg gcgcagggaa gggaaccgtc 60
gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc ggggccggct cacttgctc 120
tccctacgca g 131

<210> 42
<211> 89
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(89)
<223> 4th MN intron

<400> 42
gtgagcgcgg actggccgag aaggggcaaa ggagcggggc ggacgggggc cagagacgtg 60
gccctctcct accctcgtgt ccttttcag 89

<210> 43
<211> 1400
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1400)
<223> 5th MN intron

<400> 43

gtaccagatc	ctggacaccc	cctactcccc	gctttcccat	cccatgctcc	tcccggactc	60
tatcgtggag	ccagagaccc	catcccagca	agctcactca	ggcccctggc	tgacaaactc	120
attcacgcac	tgtttggtca	tttaacaccc	actgtgaacc	aggcaccagc	ccccaacaag	180
gattctgaag	ctgtaggtcc	ttgcctctaa	ggagcccaca	gccagtgggg	gaggctgaca	240
tgacagacac	ataggaagga	catagtaaag	atgggtggta	cagaggaggt	gacacttaaa	300
gccttcactg	gtagaaaaga	aaaggaggtg	ttcattgcag	aggaaacaga	atgtgcaaag	360
actcagaata	tggcctatct	agggaatggc	tacatacacc	atgattagag	gaggcccagt	420
aaaggggaag	gatgggtgaga	tgcctgctag	gttcactcac	tcacttttat	ttatttatct	480
atcttttttg	cagtctctct	gtcgcccagg	ctggagtgcg	gtgggtgtgat	cttgggtcac	540
tgcaacttcc	gcctcccggg	ttcaagggat	tctcctgcct	cagcttcctg	agtagctggg	600
gttacagggt	tgtgccacca	tgcccagcta	atcttttttt	gtatttttag	tagacagggg	660
ttcaccatgt	tggtcaggct	ggtctcaaac	tcttggcctc	aagtgatccg	cctgactcag	720
cctaccaaag	tgctgattac	aagtgtgagc	caccgtgccc	agccacactc	actgattctt	780
taatgccagc	cacacagcac	aaagttcaga	gaaatgcctc	catcatagca	tgtcaatatg	840
ttcatactct	taggttcatg	atgttcttaa	cattaggttc	ataagcaaaa	taagaaaaaa	900
gaataataaa	taaaagaagt	ggcatgtcag	gacctcacct	gaaaagccaa	acacagaatc	960
atgaagggtg	atgcagaggt	gacaccaaca	caaagggtga	tatatggttt	cctgtgggga	1020
gtatgtacgg	aggcagcagt	gagtgaagct	gcaaacgtca	gaagggcacg	ggtcactgag	1080
agcctagtat	cctagtaaag	tgggtctctc	ccctctctct	ccagcttggt	attgaaaacc	1140
agtccacca	gcttggttgg	tgcacagca	agagtacata	gagtttgaaa	taatacatag	1200
gattttaaga	gggagacact	gtctctaaaa	aaaaaaacaa	cagcaacaac	aaaaagcaac	1260
aaccattaca	atcttatgtt	ccctcagcat	tctcagagct	gaggaatggg	agaggactat	1320
gggaaccccc	ttcatgttcc	ggccttcagc	catggccctg	gatacatgca	ctcatctgtc	1380
ttacaatgtc	attccccag					1400

<210> 44

<211> 1334

<212> DNA

<213> HUMAN

<220>

<221> intron

<222> (1)..(1334)

<223> 6th MN intron

<400> 44

gtcagtttgt	tgggtctggc	actaatctct	gtggcctagt	tcataaagaa	tcaccctttg	60
gagcttcagg	tctgaggctg	gagatgggct	ccctccagtg	caggagggat	tgaagcatga	120
gccagcgctc	atcttgataa	taaccatgaa	gctgacagac	acagttaccc	gcaaacggct	180
gcctacagat	tgaaaaccaa	gcaaaaaccg	ccgggcacgg	tggctcacgc	ctgtaatccc	240
agcacttttg	gaggccaagg	caggtggatc	acgaggtcaa	gagatcaaga	ccatcctggc	300
caacatgggt	aaaccccatc	tctactaaaa	atacgaaaaa	atagccaggc	gtgggtggcg	360
gtgcctgtaa	tcccagctac	tggggaggct	gaggcaggag	aatggcatga	accggggagg	420
cagaagttgc	agtgagccga	gatcgtgcca	ctgcactcca	gcctgggcaa	cagagcgaga	480
ctcttgtctc	aaaaaaaaaa	aaaaaaaaaa	aaaccaagca	aaaacccaaa	tgagacaaaa	540
aaaacaagac	caaaaaatgg	tgtttggaag	ttgtcaagg	caagtctgga	gagctaaact	600
ttttctgaga	actgtttatc	tttaataagc	atcaaatatt	ttaactttgt	aaatactttt	660
gttggaatc	gttctcttct	tagtcactct	tgggtcattt	taaatctcac	ttactctact	720
agacctttta	ggtttctgct	agactaggtg	gaactctgcc	tttgcatttc	ttgtgtctgt	780

tttgtatagt	tatcaatatt	catatatttatt	tacaagttat	tcagatcatt	ttttcttttc	840
tttttttttt	tttttttttt	ttttacatct	ttagtagaga	cagggtttca	ccatattggc	900
caggctgctc	tcaaactcct	gaccttgtga	tccaccagcc	tcggcctccc	aaagtgctgg	960
gattcatttt	ttctttttta	tttgctctgg	gcttaaactt	gtggcccagc	actttatgat	1020
ggtacacaga	gttaagagtg	tagactcaga	cggctcttct	tctttccttc	tcttccttcc	1080
tcccttcctc	cccaccttcc	cttctctcct	tcctttcttt	cttcctctct	tgcttcctca	1140
ggcctcttcc	agttgctcca	aagccctgta	cttttttttg	agttaacgtc	ttatgggaag	1200
ggcctgcact	tagtgaagaa	gtggtctcag	agttgagtta	ccttggcttc	tgggaggtga	1260
aactgtatcc	ctataccctg	aagctttaag	ggggtgcaat	gtagatgaga	ccccaacata	1320
gacctcttc	acag					1334

<210> 45
 <211> 512
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(512)
 <223> 7th MN intron

<400> 45	
gtgggcctgg	ggtgtgtgtg gacacagtgg gtgcggggga aagaggatgt aagatgagat 60
gagaaacagg	agaagaaaga aatcaaggct gggctctgtg gcttacgcct ataatcccac 120
cacgttgga	ggctgaggtg ggagaatggg ttgagcccag gagttcaaga caaggcgggg 180
caacatagtg	tgaccccatc tctacaaaa aaacccaac aaaacaaaa atagccgggc 240
atggtggtat	gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300
ttccaggagt	ttgagactgc agtgagctat gatcccacca ctgcctacca tctttaggat 360
acattttatt	atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420
tggagccctg	aggtgctggg tgtgagctgg cctgggaccc ttgtttcctg tcatgccatg 480
aaccaccca	cactgtccac tgacctcct ag 512

<210> 46
 <211> 114
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(114)
 <223> 8th MN intron

<400> 46	
gtacagcttt	gtctggtttc cccccagcca gtagtccctt atcctcccat gtgtgtgcc 60
gtgtctgtca	ttggtgggtc cagcccgct ctcacatctc ctttttctct ccag 114

<210> 47
 <211> 617

<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(617)
<223> 9th MN intron

<400> 47
gtgagtctgc ccctcctctt ggctcctgatg ccaggagact cctcagcacc attcagcccc 60
agggctgctc aggaccgcct ctgctccctc tccttttctg cagaacagac cccaacccca 120
atattagaga ggcagatcat ggtggggatt cccccattgt cccagaggc taattgatta 180
gaatgaagct tgagaaatct ccagcatcc ctctcgcaa agaatcccc cccctttttt 240
taaagatagg gtctcactct gtttgcccca ggctggggtg ttgtggcacg atcatagctc 300
actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360
ggactgtagg catgagccac tgtgcctggc cccaaacggc ctttttactt ggcttttagg 420
aagcaaaaac ggtgcttata ttacccttcc tcgtgtatcc accctcatcc cttggctggc 480
ctcttctgga gactgaggca ctatggggct gcctgagaac tcggggcagg ggtgggtggag 540
tgcactgagg caggtgttga ggaactctgc agaccctct tccttcccaa agcagccctc 600
tctgctctcc atcgag 617

<210> 48
<211> 130
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

<400> 48
gtattacact gaccctttct tcaggcaca gcttccccca cccttgtgga gtcacttcat 60
gcaaagcgca tgcaaataag ctgctcctgg gccagtttcc tgattagcct ttcctgttgt 120
gtacacacag 130

<210> 49
<211> 1401
<212> DNA
<213> HUMAN

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctactgcaa 60
cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120
tacaggcatg cgccaccacg cccggctaata ttttgtattt ttagtagaga cggggtttcg 180
ccatgttggc caggctggc tcgaactcct gatctcagg gatccaacca ccctggcctc 240
ccaaagtgtc gggattatag gcgtgagcca cagcgcctgg cctgaagcag ccactcactt 300
ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc caccagctg 360
cgggtgttgag tttgggtgag gtctcctgtg ctttgcacct ggcccgtta aggcatttgt 420

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taccgtaat gctcctgtaa ggcattctgcg tttgtgacat cgtttttggtc gccaggaagg 480
gattggggct ctaagcttga gcggttcac cttttcattt atacagggga tgaccagagt 540
cattggcgct atggaggtga gacacccacc cgctgcacag acccaatctg ggaacccagc 600
tctgtggatc tcccctacag ccgtccctga aacttggtcc cgggcgtccc acccgccgcc 660
caccgtccca cccctcacc ttttctaccc gggttcccta agttcctgac ctaggcgtca 720
gacttcctca ctatactctc ccaccccagg cgacccgccc tggccccggg tgtccccagc 780
ctgcgcgggc cgcttccagt ccccggtgga tatccgcccc cagctcgccg ccttctgccc 840
ggccctgcgc cccctggaac tcctgggctt ccagctcccg ccgctcccag aactgcgcct 900
gcgcaacaat ggccacagtg gtgagggggt ctccccgccg agacttgggg atggggcggg 960
gcgcagggaa gggaaccgtc ggcagtgcc tgccccgggg ttgggctggc cctaccgggc 1020
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atggctctgg gtcccgggcg ggagtaccgg gctctgcagc tgcattctgca ctggggggct 1140
gcaggtcgtc cgggctcgga gcacactgtg gaaggccacc gtttccctgc cgaggtgagc 1200
gcggaactgg cgagaagggg caaaggagcg gggcggacgg gggccagaga cgtggccctc 1260
tcctaccctc gtgtcctttt cagatccacg tggttcacct cagcaccgcc tttgccagag 1320
ttgacgaggc cttggggcgc ccgggaggcc tggccgtgtt ggccgccttt ctggagggtac 1380
cagatcctgg acacccccta c 1401

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<210> 50
 <211> 59
 <212> PRT
 <213> HUMAN

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<400> 50
Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
  1              5              10              15

Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
      20              25              30

Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
  35              40              45

Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
  50              55

```

<210> 51
 <211> 257
 <212> PRT
 <213> HUMAN

```

<400> 51
Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
  1              5              10              15

Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
      20              25              30

```


Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
 35 40 45
 Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
 50 55 60
 Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
 65 70 75 80
 Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly
 85 90 95
 Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe
 100 105 110
 Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
 115 120 125
 Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe
 130 135 140
 Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser
 145 150 155 160
 Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly
 165 170 175
 Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln
 180 185 190
 Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp
 195 200 205
 Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr
 210 215 220
 Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
 225 230 235 240
 Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
 245 250 255

Pro

<210> 52
 <211> 20
 <212> PRT
 <213> HUMAN

<400> 52

Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
1 5 10 15

Phe Leu Val Gln
20

<210> 53

<211> 25

<212> PRT

<213> HUMAN

<400> 53

Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1 5 10 15

Pro Ala Glu Val Ala Glu Thr Gly Ala
20 25

<210> 54

<211> 59

<212> PRT

<213> HUMAN

<400> 54

Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
1 5 10 15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
20 25 30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
35 40 45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
50 55

<210> 55

<211> 470

<212> RNA

<213> HUMAN

<400> 55

cauggccccc auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60
gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120
cugcaaaagg ggcucugug agucagccug cuccccucca ggcuugcucc uccccaccc 180
agcucucguu uccaaugcac guacagcccc uacacaccgu gugcugggac accccacagu 240
cagccgcaug gcuccccugu gccccagccc cuggcucccu cuguugauc cggccccugc 300

```

uccaggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucacca 360
gagguugccc cggaugcagg aggauucucc cuugggagga ggcucuucug gggaagauga 420
cccacugggc gaggaggauc ugcccaguga agaggauuca cccagagagg          470

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<210> 56
<211> 292
<212> DNA
<213> HUMAN

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<400> 56
gttttttttga gacggagtct tgcattctgtc atgcccaggc tggagtagca gtggtgccat 60
ctcggctcac tgcaagctcc acctcccgag ttcacgccat tttcctgcct cagcctcccg 120
agtagctggg actacaggcg cccgccacca tgcccggcta attttttgta tttttggtag 180
agacgggggtt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240
gcctcggcct cccaaagtgc tgggattaca ggtgtgagcc accgcacctg gc          292

```

```

<210> 57
<211> 262
<212> DNA
<213> HUMAN

```

```

<400> 57
tttctttttt gagacagggt cttgctctgt caccaggcc agagtgcatt ggtacagtct 60
cagctcactg cagcctcaac cgctcggct caaacattca tccatttca gcctcctgag 120
tagctgggac tacaggcaca tgccattaca cctgggtaat ttttttgat ttctagtaga 180
gacagggttt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240
cacctcagcc tcccaaatg ag          262

```

```

<210> 58
<211> 2501
<212> DNA
<213> HUMAN

```

```

<220>
<221> misc_feature
<222> (1)..(2501)
<223> region 5' to transcription initiation site as determined by RNase
protection assay (nucleotide 3507 of Figures 2A-2F and of SEQ ID NO: 5),
corresponding to region of SEQ ID NO: 5 and Figures 2A-2F from nucleotide
(7) to nucleotide (2507), in which region some regulatory elements are
probably situated.

```

```

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of base at position 1968, which is the same unknown base as
that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic
sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and

```

unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5' region flanking the transcription initiation site (3507) as determined by RNase protection assay.

<400> 58

tggtgactcg	tgaccttacc	cccaaccctg	tgctctctga	aacatgagct	gtgtccactc	60
agggttaaat	ggattaaggg	cggtgcaaga	tgtgctttgt	taaacagatg	cttgaaggca	120
gcatgctcgt	taagagtcac	caccaatccc	taatctcaag	taatcaggga	cacaaacact	180
gcggaaggcc	gcagggtcct	ctgcctagga	aaaccagaga	cctttgttca	cttgtttata	240
tgaccttccc	tccactattg	tccatgaccc	tgccaaatcc	ccctctgtga	gaaacaccca	300
agaattatca	ataaaaaaat	aaattttaaaa	aaaaaataca	aaaaaaaaaa	aaaaaaaaaa	360
aaaagactta	cgaatagtta	ttgataaatg	aatagctatt	ggtaaagcca	agtaaatgat	420
catattcaaa	accagacggc	catcatcaca	gctcaagtct	acctgatttg	atctctttat	480
cattgtcatt	ctttggattc	actagattag	tcatcatcct	caaaattctc	ccccagttc	540
taattacgtt	ccaaacattt	aggggttaca	tgaagcttga	acctactacc	ttctttgctt	600
ttgagccatg	agttgtagga	atgatgagtt	tacaccttac	atgctgggga	tttaatttaa	660
ctttacctct	aagtcagttg	ggtagccttt	ggcttatttt	tgtagctaata	tttgtagtta	720
atggatgcac	tgtgaatctt	gctatgatag	ttttcctcca	cactttgcca	ctaggggtag	780
gtaggtactc	agttttcagt	aattgcttac	ctaagaccct	aagccctatt	tctctgttac	840
tggcctttat	ctgtaatatg	ggcatattta	atacaatata	atttttggag	tttttttggt	900
tgtttgtttg	tttggttttt	tgagacggag	tcttgcatct	gtcatgccca	ggctggagta	960
gcagtgggtg	catctcggct	cactgcaagc	tccacctccc	gagttcacgc	cattttcctg	1020
cctcagcctc	ccgagtagct	gggactacag	gcgcccgcga	ccatgcccg	ctaatttttt	1080
gtattttttg	tagagacggg	gtttcaccgt	gtagccaga	atgggtctcg	tctcctgact	1140
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ctggccaatt	ttttgagtct	tttaaagtaa	aaatatgtct	tgtaaagctg	taactatggt	1260
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ttggtaccac	ttggatcata	agtggaaaaa	cagtcaagaa	attgcacagt	aatacttggt	1500
tgtaaagagg	atgattcagg	tgaatctgac	actaagaaac	tcccctacct	gaggtctgag	1560
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taatctcaat	tctgtcagaa	ttggtacaag	aaatagctgc	tatgtttctt	gacattccac	1920
ttggtaggaa	ataagaatgt	gaaactcttc	agttgggtgtg	tgccctngt	ttttttgcaa	1980
tttccttctt	actgtgttaa	aaaaaagtat	gatcttgctc	tgagaggtga	ggcattctta	2040
atcatgatct	ttaaagatca	ataatataat	cctttcaagg	attatgtctt	tattataata	2100
aagataaatt	gtctttaaca	gaatcaataa	tataatccct	taaaggatta	tatctttgct	2160
gggcgcagtg	gctcacacct	gtaatcccag	cactttgggt	ggccaagggtg	gaaggatcaa	2220
atttgcttac	ttctatatta	tcttctaaag	cagaattcat	ctctcttccc	tcaatatgat	2280
gatattgaca	gggtttgccc	tcactcacta	gattgtgagc	tcctgctcag	ggcaggtagc	2340
gttttttggt	tttggttttg	tttttctttt	ttgagacagg	gtcttgctct	gtcaccacag	2400
ccagagtgca	atggtacagt	ctcagctcac	tgcagcctca	accgcctcgg	ctcaaaccat	2460
catcccattt	cagcctcctg	agtagctggg	actacaggca	c		2501

<210> 59

<211> 292

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)

<400> 59
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gtagctggga ctacaggcgc ccgccaccat gcccggttaa ttttttgtat ttttggtaga 180
gacgggggtt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccacccg 240
cctcggcctc ccaaagttct gggattacag gtgtgagcca ccgcacctgg cc 292

<210> 60
<211> 262
<212> DNA
<213> HUMAN

<400> 60
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agctcactgc agcctcaacc gcctcggctc aaaccatcat cccatttcag cctcctgagt 120
agctgggact acaggcacat gccattacac ctgggctaatt tttttgtatt tctagtagag 180
acagggtttg gccatgttgc ccgggctggg ctcgaaactcc tggactcaag caatccaccc 240
acctcagcct cccaaaatga gg 262

<210> 61
<211> 294
<212> DNA
<213> HUMAN

<400> 61
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cggtcactgc caacctccac ctcccgggtt caagtatttc ttctgcctca gcctctagcc 120
aagtagctgc gattacaggc atgcgccacc acgcccggct aattttttgta ttttttagtag 180
agacgggggtt tcgccaatgtt ggtcaggctg gtctcgaaact cctgatctca ggtgatccaa 240
ccacctggtc ctcccaaagt gctgggatta taggcgtgag ccacagcgcc tggc 294

<210> 62
<211> 276
<212> DNA
<213> HUMAN

<400> 62
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tccgcctccc gggttcaagg gattctcctg cctcagcttc ctgagtagct ggggttacag 120
gtgtgtgcca ccatgccag ctaatttttt tttgtatttt tagtagacag ggtttcacca 180
tggtgggtcag gctgggtctc aactcctggc ctcaagtgat ccgcctgact cagcctacca 240

aagtgtgat tacaagtgtg agccaccgtg cccagc

276

<210> 63
<211> 289
<212> DNA
<213> HUMAN

<400> 63
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tcacgagggtc aagagatcaa gaccatcctg gccaacatgg tgaaacccca tctctactaa 120
aaatacgaaa aaatagccag gcgtgggtggc ggggtgcctgt aatcccagct actcgggagg 180
ctgaggcagg agaatggcat gaaccggga ggcagaagtt gcagtgagcc gagatcgtgc 240
cactgcactc cagcctgggc aacagagcga gactcttgtc tcaaaaaaa 289

<210> 64
<211> 298
<212> DNA
<213> HUMAN

<400> 64
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atggtttgag cccaggagtt caagacaagg cggggcaaca tagtgtgacc ccattctctac 120
caaaaaaacc ccaacaaaac caaaaatagc cgggcatggt ggtatgcggc ctagtcccag 180
ctactcaagg aggctgaggt gggaagatcg cttgattcca ggagtttgag actgcagtga 240
gctatgatcc caccactgcc taccatcttt aggatacatt tattttattta taaaagaa 298

<210> 65
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<400> 65
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<211> 83
<212> DNA
<213> HUMAN

<400> 66
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aggcatgagc cactgtgcct ggc 83

<210> 67
<211> 11

<212> DNA
<213> HUMAN

<400> 67
agaaggtaag t 11

<210> 68
<211> 11
<212> DNA
<213> HUMAN

<400> 68
tggaggtgag a 11

<210> 69
<211> 11
<212> DNA
<213> HUMAN

<400> 69
cagtcgtgag g 11

<210> 70
<211> 11
<212> DNA
<213> HUMAN

<400> 70
ccgaggtgag c 11

<210> 71
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<212> DNA
<213> HUMAN

<400> 71
tggaggtacc a 11

<210> 72
<211> 11
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<213> HUMAN

<400> 72
ggaaggtcag t 11

<210> 73
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<212> DNA
<213> HUMAN

<400> 73
agcaggtggg c 11

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<400> 74
gccaggtaca g 11

<210> 75
<211> 11
<212> DNA
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<400> 75
tgctggtgag t 11

<210> 76
<211> 11
<212> DNA
<213> HUMAN

<400> 76
cacaggtatt a 11

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<211> 11
<212> DNA
<213> HUMAN

<400> 77
atacagggga t 11

<210> 78
<211> 11
<212> DNA
<213> HUMAN

<400> 78

ccccaggcga c 11

<210> 79
<211> 11
<212> DNA
<213> HUMAN

<400> 79
acgcagtgca a 11

<210> 80
<211> 11
<212> DNA
<213> HUMAN

<400> 80
tttcagatcc a 11

<210> 81
<211> 11
<212> DNA
<213> HUMAN

<400> 81
ccccaggagg g 11

<210> 82
<211> 11
<212> DNA
<213> HUMAN

<400> 82
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<212> DNA
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<400> 83
ccctagctcc a 11

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<211> 11
<212> DNA

<213> HUMAN

<400> 84

ctccagtcga g

11

<210> 85

<211> 12

<212> DNA

<213> HUMAN

<400> 85

tcgcaggtga ca

12

<210> 86

<211> 11

<212> DNA

<213> HUMAN

<400> 86

acacagaagg g

11

<210> 87

<211> 377

<212> PRT

<213> HUMAN

<400> 87

Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
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Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
20 25 30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
35 40 45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
50 55 60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
65 70 75 80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
85 90 95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
100 105 110

Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp	115	120	125
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu	130	135	140
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	145	150	155
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala	165	170	175
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	180	185	190
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	195	200	205
Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	210	215	220
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	225	230	235
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu	245	250	255
Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro	260	265	270
Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe	275	280	285
Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile	290	295	300
Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His	305	310	315
Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	325	330	335
Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	340	345	350
Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	355	360	365
Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp								370	375	

<210> 88
 <211> 34
 <212> DNA
 <213> HUMAN

<400> 88
 tagacagatc tacgatggct cccctgtgcc ccag

34

<210> 89
 <211> 34
 <212> DNA
 <213> HUMAN

<400> 89
 attcctctag acagttaccg gctccccctc agat

34

<210> 90
 <211> 3532
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature which includes the MN gene promoter
 <222> (1)..(3532)
 <223> region including the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter, and corresponds to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
 <221> unsure what base is at position 1968
 <222> (1968)
 <223> unsure of the base at position 1968, which is the same unknown base at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence), position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That unknown base is in the region that includes the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter.

<400> 90
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 gcatgctcgt taagagtcac caccaatccc taatctcaag taatcaggga cacaaacact 180
 gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
 tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
 agaattatca ataaaaaaat aaatttataa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360
 aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
 catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480

cattgtcatt	ctttggattc	actagattag	tcatcatcct	caaaattctc	ccccaagttc	540
taattacgtt	ccaaacattt	aggggttaca	tgaagcttga	acctactacc	ttcttttgctt	600
ttgagccatg	agttgtagga	atgatgagtt	tacaccttac	atgctgggga	tttaatttaaa	660
ctttacctct	aagtcagttg	ggtagccttt	ggcttatttt	tgtagctaata	tttgtagtta	720
atggatgcac	tgtgaatcct	gctatgatag	ttttcctcca	cactttgcca	ctaggggtag	780
gtaggtactc	agttttcagt	aattgcttac	ctaagaccct	aagccctatt	tctcttgtag	840
tggcctttat	ctgtaatatg	ggcatattta	atacaatata	atttttggag	tttttttggt	900
tgtttgtttg	tttgtttttt	tgagacggag	tcttgcatct	gtcatgcca	ggctggagta	960
gcagtgggtg	catctcggct	cactgcaagc	tccacctccc	gagttcacgc	cattttcctg	1020
cctcagcctc	ccgagtagct	gggactacag	gcgcccgcga	ccatgcccgg	ctaatttttt	1080
gtattttttg	tagagacggg	gtttcaccgt	gttagccaga	atgggtctcga	tctcctgact	1140
tctgtatcca	cccgctcgg	cctcccaaag	ttctgggatt	acaggtgtga	gccaccgcac	1200
ctggccaatt	ttttgagtct	tttaaagtaa	aaatatgtct	tgtaaagctgg	taactatggg	1260
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tttccttctt	actgtgttaa	aaaaaagtat	gatcttgctc	tgagaggtga	ggcattctta	2040
atcatgatct	ttaaagatca	ataatataat	cctttcaagg	attatgtctt	tattataata	2100
aagataaatt	gtctttaaca	gaatcaataa	tataatccct	taaaggatta	tatctttgct	2160
gggcgcagtg	gctcacacct	gtaatcccag	cactttgggt	ggccaagggtg	gaaggatcaa	2220
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cctagcagcc	tgcctacct	ctttacctgc	ttcctgggtg	agtcagggat	gtatacatga	3120
gctgctttcc	ctctcagcca	gaggacatgg	ggggccccag	ctccccctgc	tttccccctc	3180
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aaagggcgct	ctgtgagtca	gcctgctccc	ctccaggctt	gctcctcccc	caccagctc	3480
tcgtttccaa	tgcacgtaca	gcccgtacac	accgtgtgct	gggacacccc	ac	3532

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<211> 204
<212> DNA
<213> HUMAN

<400> 91
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caaacctgtg agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120
ccctccaggc ttgctcctcc cccacccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg ctgggacacc ccac 204

<210> 92
<211> 132
<212> DNA
<213> HUMAN

<400> 92
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ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttggttaa cagatgcttg 120
aagcagcat gc 132

<210> 93
<211> 275
<212> DNA
<213> HUMAN

<400> 93
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acagggccag acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag 180
tcagcctgct cccctccagg cttgctcctc cccacccag ctctcgtttc caatgcacgt 240
acagcccgtc cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

<400> 94
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ccgtacacac cgtgtgctgg gacacccca 89

<210> 95
<211> 61
<212> DNA
<213> HUMAN

<400> 95
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a 61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
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acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
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Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
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Glu Asp Leu Pro
35

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<211> 6
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<400> 98
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1 5

<210> 99
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<212> PRT
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<400> 99
Glu Glu Asp Leu
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<210> 100
<211> 5
<212> PRT
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<400> 100
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1 5

<210> 101
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<212> PRT
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<400> 101
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<210> 102
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<212> PRT
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<400> 102
Glu Glu Asp Leu Pro Ser Glu
1 5

<210> 103
<211> 6
<212> PRT
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<400> 103
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1 5

<210> 104
<211> 22
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Ser Glu Glu Asp Ser Pro
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<210> 105
<211> 25
<212> PRT
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1 5 10 15
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<210> 106
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<210> 107
<211> 7
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<400> 107
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1 5

<210> 108
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1 5

<210> 109
<211> 7
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<213> HUMAN

<210> 111
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 <212> DNA
 <213> HUMAN

 <400> 111
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 <210> 112
 <211> 23
 <212> DNA
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 <400> 112
 aggcttgctc ctccccacc cag 23

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 <400> 113
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 <210> 114
 <211> 20
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 <400> 114
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 <210> 115
 <211> 26
 <212> DNA
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 <400> 115
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 <210> 116
 <211> 15
 <212> PRT
 <213> HUMAN

 <400> 116

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<210> 117
<211> 34
<212> DNA
<213> HUMAN

<400> 117
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34

<210> 118
<211> 15
<212> PRT
<213> HUMAN

<400> 118
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
1 5 10 15

<210> 119
<211> 12
<212> PRT
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<400> 119
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1 5 10

<210> 120
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1 5 10

<210> 121
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<212> PRT
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Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10

<210> 122
<211> 12
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<400> 122
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1 5 10

<210> 123
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<400> 123
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1 5 10

<210> 124
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<212> PRT
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<400> 124
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1 5 10

<210> 125
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<210> 126
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<210> 128
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Ala Glu Asp Leu Pro Gly Glu Glu Ala
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<400> 129
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